

FIGURE

1a 3b

C1e/C1a	
HASP-2	126GKQKPEVFCALASQFPOETANDGERKNTLTAPPQYRLALYTHFOELSHLCEYDFVLSGACVLAFLCQSBSTOTERAPQADT 50
HASP-1	HTVELNHNFOQIGSPGYPOSFSDSEVTWNITVPDGFRIKLYTHFNLESSTLCYDYVKVETEDQVLATPQCKATDTOTETQPGQEV 47
C1e	SIDIPQKLPGVETSPLPSPVPMFETTTVTFTOTRKLVPQDPLESEDCFTDYVKLSADKESLGRFOQLGSPFGNPPGKKE 47
C1a	EPHYGELISPHYQATSEVERKNDVEPDYQINLYTHLOISELSEKAYDSVQIISGOTERKLGQGRSSNPHSPIVEK 43
EGP	
HASP-2	FYSLGSLQITTESDYSEERETGSAFYAASDIDEGVAPGEAPTCDHKGHNLGSPYCSERACTVLRNKAQCALCS 170
HASP-1	VLEPGSPHSTIPRSDTSEERETGSAFYAASDIDEGVAPGEAPTCDHKGHNLGSPYCSERACTVLRNKAQCALCS 167
C1e	FNQGNHLLTFTDFTSEEDNTIMFYKFLATYQAVDLOECASREKGEEDPOPGQHLQMYVGGYFCQUPYBLOEDRHSQACGS 177
C1a	FGVPMKLVIFKSDPSEERETGSAFYAASDIDEGVAPGEAPTCDHKGHNLGSPYCSERACTVLRNKAQCALCS 163
C1e/C1a	
HASP-2	QGVFTQSGELSSPEYPRPYKLSNCTISLSEQSPVILQVESPQVETNPEELGPTDPLKIGTDASSHQPPQKTLPHR 125
HASP-1	DNLFQRTQVITSPOFPHYKESBOLYILEEGPVMKLOFEDFOIEDNPEVPCFTDYVKVETEDQVLATPQCKATDTOTETQPGQEV 123
C1e	SELVTEASQYISSEYPRPYKLSNCTISLSEQSPVILQVESPQVETNPEELGPTDPLKIGTDASSHQPPQKTLPHR 123
C1a	QGVFTALDGIASPHYKPYKLSNCTISLSEQSPVILQVESPQVETNPEELGPTDPLKIGTDASSHQPPQKTLPHR 120
CCP-1	
HASP-2	HTVITFTDSESGDQNKINHTSTAGPCTVPHAPPHQVSPVQKYLKQSPFPQSTOVELLQHLPLKSTAVQDQDCAWDRPFA 345
HASP-1	HSVLIPMNSGSDQNKINHTSTAGPCTVPHAPPHQVSPVQKYLKQSPFPQSTOVELLQHLPLKSTAVQDQDCAWDRPFA 342
C1e	NAVOLLPTDSESGDQNKINHTSTAGPCTVPHAPPHQVSPVQKYLKQSPFPQSTOVELLQHLPLKSTAVQDQDCAWDRPFA 350
C1a	NALDITFTDSESGDQNKINHTSTAGPCTVPHAPPHQVSPVQKYLKQSPFPQSTOVELLQHLPLKSTAVQDQDCAWDRPFA 338
CCP-2	
HASP-2	QSVVQGGPDDLPSGHVEYITGQVYKAVIQYSGEETPYTHKVNQKYVQADGPTVSEKELPVCEPVQGLSARTT 426
HASP-1	QSVVQGGPDDLPSGHVEYITGQVYKAVIQYSGEETPYTHKVNQKYVQADGPTVSEKELPVCEPVQGLSARTT 426
C1e	QSVVQGGPDDLPSGHVEYITGQVYKAVIQYSGEETPYTHKVNQKYVQADGPTVSEKELPVCEPVQGLSARTT 443
C1a	QSVVQGGPDDLPSGHVEYITGQVYKAVIQYSGEETPYTHKVNQKYVQADGPTVSEKELPVCEPVQGLSARTT 419
serine protease	
HASP-2	QGRVGGQKAKPGDPFQVQVLIQGTAAAGALLYDNVLTAAHAYTEQKNDASALDITRGTLRSLPHYQTHSEAVPIHQ 507
HASP-1	QGRVGGQKAKPGDPFQVQVLIQGTAAAGALLYDNVLTAAHAYTEQKNDASALDITRGTLRSLPHYQTHSEAVPIHQ 515
C1e	QGRVGGQKAKPGDPFQVQVLIQGTAAAGALLYDNVLTAAHAYTEQKNDASALDITRGTLRSLPHYQTHSEAVPIHQ 523
C1a	QGRVGGQKAKPGDPFQVQVLIQGTAAAGALLYDNVLTAAHAYTEQKNDASALDITRGTLRSLPHYQTHSEAVPIHQ 498
FONDIAL	
HASP-2	YTHDAGFONDIALKLNHNVINHTIPCLPRKEALSFTMTDDIGTASGGLTQRFPLAHLNHYDIPVQKQCTAAYEK 589
HASP-1	VKHTTLKPYDQNTFONDIALVELLESPLVNAFNPICLPQPGQKQAVVSVQWQKQFLQFPETLHEIIPVQKQCTAAYEK 599
C1e	SVHPDYKQDSEYFONDIALVELLESPLVNAFNPICLPQPGQKQAVVSVQWQKQFLQFPETLHEIIPVQKQCTAAYEK 608
C1a	WKLLEVPEGRTHFONDIALVRLKQPVKMGPTVSPICLPQTSQSYVLMQDGLGISNGATEKRDRAVRLKAALPVAPLKKQKQVKE 586
STER	
HASP-2	PPYPRG3VTANMLCAGLESQGGKSGGSGGALVFLDSSTERFVQGVIVSGSNDEAGQYGVYTKVINYIPWNIETISOP 671
HASP-1	APLKKKYTRNMLCAGLESQGGKSGGSGGALVFLDSSTERFVQGVIVSGSNDEAGQYGVYTKVINYIPWNIETISOP 680
C1e	QKVRMDVFSQNMPCAGHPSLKQDAGSGGSGGALVFLDSSTERFVQGVIVSGSNDEAGQYGVYTKVINYIPWNIETISOP 688
C1a	KPTADALVYVTPNMLCAGLESQGGKSGGSGGALVFLDSSTERFVQGVIVSGSNDEAGQYGVYTKVINYIPWNIETISOP 673

FIGURE

2

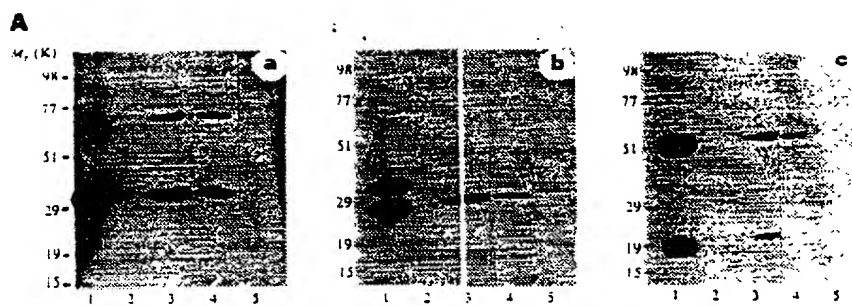
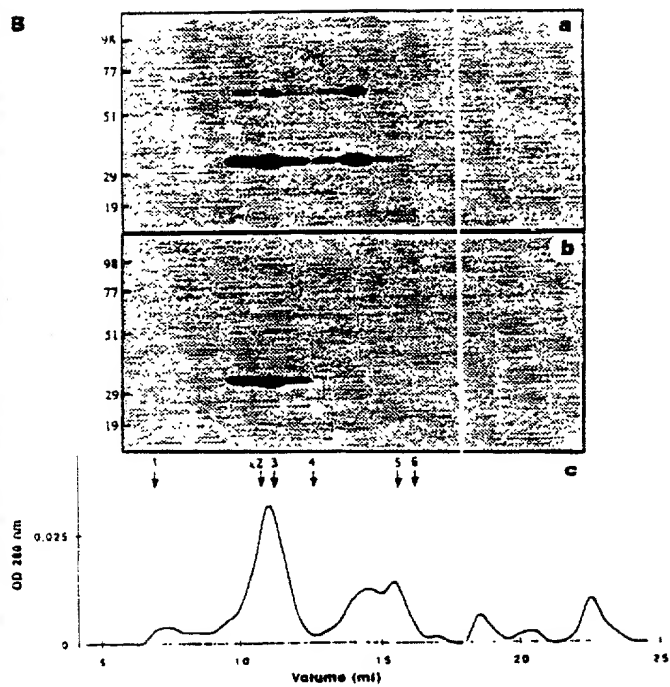
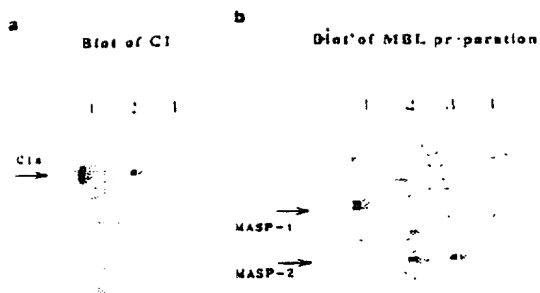


FIGURE 3A



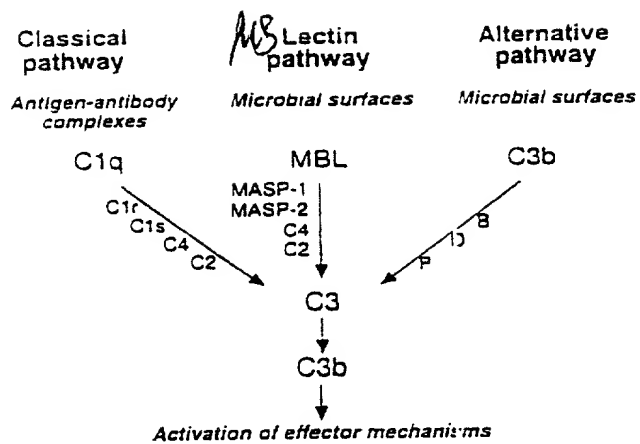
FIGURE

3b



FIGURE

4 a & b



FIGURE

5

